

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/718, 834A
Source: IFW16
Date Processed by STIC: 9-7-05

ENTERED



IFW16

RAW SEQUENCE LISTING

DATE: 09/07/2005

PATENT APPLICATION: US/10/718,834A

TIME: 14:36:40

Input Set : A:\Substitute Sequence Listing.ST25.txt

Output Set: N:\CRF4\09072005\J718834A.raw

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3 <110> APPLICANT: Wyeth
4      O'Toole, Margot
5      Mounts, William M
6      Shojaee, Negin
8 <120> TITLE OF INVENTION: COMPOSITION AND METHOD FOR TREATING LUPUS NEPHRITIS
10 <130> FILE REFERENCE: 031896-091000
12 <140> CURRENT APPLICATION NUMBER: US 10/718,834A
13 <141> CURRENT FILING DATE: 2003-11-21
15 <150> PRIOR APPLICATION NUMBER: US 60/428,065
16 <151> PRIOR FILING DATE: 2002-11-21
18 <160> NUMBER OF SEQ ID NOS: 21
20 <170> SOFTWARE: PatentIn version 3.3
22 <210> SEQ ID NO: 1
23 <211> LENGTH: 3652
24 <212> TYPE: DNA
25 <213> ORGANISM: Homo sapiens
27 <400> SEQUENCE: 1
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30 tcctcccagc atccagaaag tcccaggctg cccaaccctc tctgggacag aggaaaaatt      120
32 ggcaagggtg aaggtcacca gcacattcag gatttctctc aaaagtccca tctgccgtct      180
34 attgtggtgg aatccagtga ggtgaatgaa gagagtgggg atctccattt gccccatgag      240
36 gagctgctgc tgctcactga tggtaggaa gaggatgctg aggccttctt ccaagaccaa      300
38 agtgaagagc caggggcggc acgtcccat catcaggctc ggcaagtgga gcattcgacg      360
40 cagcgcggcc atctggagat tcgggagctg aagaagaagc tgttcaaacg ccggcgggtg      420
42 ttgaatcggg agcggcgctc gaggcaccgg gtggtcgggg ctgtgataga ccaagggtg      480
44 atcacgcggc accacctcaa gaagcgggct gctcaggagc tgtcccagga aatcaaggct      540
46 tttctgactg gcgtagacct cattctgggc caccaactct cagcccggga acatgctcgc      600
48 tgtggtcttc tcctgctccg ttctttgcca cctgctcggg ctgctgtgct tgaccacttg      660
50 agaggtgtct ttgatgagag tgtccgggcc cacctggctg ccctggatga aacctctgtg      720
52 gctggtccac ctcacctccg tccacctcca ccctctcatg tccctgctgg tggacctggt      780
54 cttagaggatg tggttcagga agtgacagc gtgctgtctg agtttatccg ggccaaccca      840
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58 acgtactcag gccagcacca gcgtgttccc cagcgtactg gcgctcttaa tgaactgcta      960
60 cagctgtgga tgggtttagt ggccacgcgt acattaatgg acatctatgt gcagtgcctc      1020
62 tcggctctca ttggtagctg cccagatgcg tgtgtggatg ccttgctgga tacctctggt      1080
64 cagcattctc cacactttga ctgggttggt gcacatattg gtcctctttt tcctggcacc      1140
66 atcatttccc gggttctctc ctgtggcctt aaggactttt gtgtccatgg tggggctgga      1200
68 ggtggagctg gcagtatggt tggaaagctc tctcagacc cctctacaga ccccttcctt      1260
70 ggaatccctg ccattctcgc ggagaaacgg gtgcccaaga ttgcctcagt tgtaggcatc      1320
72 ctaggtcacc tggcctcccg ccacggagat agcatccgac gggagctcct gcgaatgttc      1380
74 catgatagcc tggcaggggg atctggaggc cgcagtgggg accctccctt tcaggccacg      1440
76 gttccgttcc tactgcagct ggcagtcagt tcaccagctt tgctgggcac tgtctctgga      1500
78 gagcttgtgg attgcctcaa gccccagct gtgctgagcc agctgcagca acaccttcaa      1560

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80 ggattccccc gagaggagct ggacaacatg ttgaacctgg ctgtgcacct ggtgagccag 1620
82 gcctctgggg caggtgccta ccgcttgctg cagttcctgg tggacacagc tatgcctgct 1680
84 tcggtcatta ccaccaggg cctggctgtg ccagacaccg tgcgtgaggc ttgtgaccgg 1740
86 ctaatccagc tgctgtgctg gcacctgcaa aaactgggtc atcaccgggg agggctctct 1800
88 ggggaagggg tgctaggccc gccccacct ccccgcttgg tgcctttttt agatgcgctc 1860
90 aaaaaccatg ttggagagct gtgtggagag acgttacgat tggaacggaa gcgcttcctc 1920
92 tggcagcacc agctcttggg cctgctgtct gtctataccc ggcctagctg tggacctgag 1980
94 gccttggggc atctgctgag ccgagcccga agccctgaag agttgagttt ggccacccag 2040
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102 cactttgggg aatctgcctc agcccatctg tctgacctgg ctctctctct gctacatcct 2280
104 gaggaggaag tagctgaagc tgctgcctct ctcttgcca tttgtccctt tcttcttgaa 2340
106 gccttatccc cctcccagct cctgggactg gtaagggtcg gggtgacccg cttctttgcc 2400
108 tctctgaggc tgcattggacc cccaggtgtg gcctcagcct gtcagcttct caccgcctg 2460
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120 agcctcctca gcctcctggt tcaactgctg agtgccccag ggggcactga atgtggggaa 2820
122 tgctgggggg caccatctt gagtccagag gcagccaaag cagtggcagt gaccttggtg 2880
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128 tttgagctgt taaagctggt agcagctgca cccccagccc tgtgctactg ttccgtgctg 3060
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132 acccactccc cctggcacct ggaggcatcc tgcaccttag tggctgtcat ggctgaggga 3180
134 agcctcctgc ctccggccct gggtaatatg catgaagtat ttagccaact ggcacctttc 3240
136 gaggtgcgtc tgctgctgct cagtgtctgg ggttttctcc gggagcatgg gcccttgctc 3300
138 cagaagtcca tcttccaatc agagcggggt cgcttcattc gggacttctc cagggggggt 3360
140 ggaggtgagg gtggacccca tctggctgtg ctgcacagtg tcctccaccg caacatcgac 3420
142 cgcctaggtc ttttctctgg ccgtttccag gcaccttcac cgtccactct ccttcgacag 3480
144 gggacgtagc cttttcttgc tctggaagcc cagggagggt gagcagtgag agaggggaagg 3540
146 gactaacgtg ctccggaagg gtggaggttt ctcttctaag tccttggtct aaagagcgct 3600
148 gtcacttttt tctctccac tttttttttt ctaaataaaa tttgccaact tg 3652

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151 <210> SEQ ID NO: 2

152 <211> LENGTH: 1162

153 <212> TYPE: PRT

154 <213> ORGANISM: Homo sapiens

156 <400> SEQUENCE: 2

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158 Met Ala Leu Val Pro Gly Arg Ser Lys Glu Asp Gly Leu Trp Thr Arg
159 1 5 10 15
162 Asn Ser Pro Gly Ser Ser Gln His Pro Glu Ser Pro Arg Leu Pro Asn
163 20 25 30
166 Pro Leu Trp Asp Arg Gly Lys Ile Gly Lys Val Glu Gly His Gln His
167 35 40 45
170 Ile Gln Asp Phe Ser Gln Lys Ser His Leu Pro Ser Ile Val Val Glu
171 50 55 60
174 Ser Ser Glu Val Asn Glu Glu Ser Gly Asp Leu His Leu Pro His Glu

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175 65              70              75              80
178 Glu Leu Leu Leu Leu Thr Asp Gly Glu Glu Glu Asp Ala Glu Ala Phe
179              85              90              95
182 Phe Gln Asp Gln Ser Glu Glu Pro Gly Ala Ala Arg Pro His His Gln
183              100              105              110
186 Ala Arg Gln Val Glu His Ser Thr Gln Arg Gly His Leu Glu Ile Arg
187              115              120              125
190 Glu Leu Lys Lys Lys Leu Phe Lys Arg Arg Arg Val Leu Asn Arg Glu
191              130              135              140
194 Arg Arg Leu Arg His Arg Val Val Gly Ala Val Ile Asp Gln Gly Leu
195 145              150              155              160
198 Ile Thr Arg His His Leu Lys Lys Arg Ala Ala Gln Glu Leu Ser Gln
199              165              170              175
202 Glu Ile Lys Ala Phe Leu Thr Gly Val Asp Pro Ile Leu Gly His Gln
203              180              185              190
206 Leu Ser Ala Arg Glu His Ala Arg Cys Gly Leu Leu Leu Leu Arg Ser
207              195              200              205
210 Leu Pro Pro Ala Arg Ala Ala Val Leu Asp His Leu Arg Gly Val Phe
211              210              215              220
214 Asp Glu Ser Val Arg Ala His Leu Ala Ala Leu Asp Glu Thr Pro Val
215 225              230              235              240
218 Ala Gly Pro Pro His Leu Arg Pro Pro Pro Pro Ser His Val Pro Ala
219              245              250              255
222 Gly Gly Pro Gly Leu Glu Asp Val Val Gln Glu Val Gln Gln Val Leu
223              260              265              270
226 Ser Glu Phe Ile Arg Ala Asn Pro Lys Ala Trp Ala Pro Val Ile Ser
227              275              280              285
230 Ala Trp Ser Ile Asp Leu Met Gly Gln Leu Ser Ser Thr Tyr Ser Gly
231              290              295              300
234 Gln His Gln Arg Val Pro His Ala Thr Gly Ala Leu Asn Glu Leu Leu
235 305              310              315              320
238 Gln Leu Trp Met Gly Cys Arg Ala Thr Arg Thr Leu Met Asp Ile Tyr
239              325              330              335
242 Val Gln Cys Leu Ser Ala Leu Ile Gly Ser Cys Pro Asp Ala Cys Val
243              340              345              350
246 Asp Ala Leu Leu Asp Thr Ser Val Gln His Ser Pro His Phe Asp Trp
247              355              360              365
250 Val Val Ala His Ile Gly Ser Ser Phe Pro Gly Thr Ile Ile Ser Arg
251              370              375              380
254 Val Leu Ser Cys Gly Leu Lys Asp Phe Cys Val His Gly Gly Ala Gly
255 385              390              395              400
258 Gly Gly Ala Gly Ser Ser Gly Gly Ser Ser Ser Gln Thr Pro Ser Thr
259              405              410              415
262 Asp Pro Phe Pro Gly Ser Pro Ala Ile Pro Ala Glu Lys Arg Val Pro
263              420              425              430
266 Lys Ile Ala Ser Val Val Gly Ile Leu Gly His Leu Ala Ser Arg His
267              435              440              445
270 Gly Asp Ser Ile Arg Arg Glu Leu Leu Arg Met Phe His Asp Ser Leu
271              450              455              460

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274 Ala Gly Gly Ser Gly Gly Arg Ser Gly Asp Pro Ser Leu Gln Ala Thr
275 465                               470           475           480
278 Val Pro Phe Leu Leu Gln Leu Ala Val Met Ser Pro Ala Leu Leu Gly
279                               485           490           495
282 Thr Val Ser Gly Glu Leu Val Asp Cys Leu Lys Pro Pro Ala Val Leu
283                               500           505           510
286 Ser Gln Leu Gln Gln His Leu Gln Gly Phe Pro Arg Glu Glu Leu Asp
287                               515           520           525
290 Asn Met Leu Asn Leu Ala Val His Leu Val Ser Gln Ala Ser Gly Ala
291                               530           535           540
294 Gly Ala Tyr Arg Leu Leu Gln Phe Leu Val Asp Thr Ala Met Pro Ala
295 545                               550           555           560
298 Ser Val Ile Thr Thr Gln Gly Leu Ala Val Pro Asp Thr Val Arg Glu
299                               565           570           575
302 Ala Cys Asp Arg Leu Ile Gln Leu Leu Leu Leu His Leu Gln Lys Leu
303                               580           585           590
306 Val His His Arg Gly Gly Ser Pro Gly Glu Gly Val Leu Gly Pro Pro
307                               595           600           605
310 Pro Pro Pro Arg Leu Val Pro Phe Leu Asp Ala Leu Lys Asn His Val
311                               610           615           620
314 Gly Glu Leu Cys Gly Glu Thr Leu Arg Leu Glu Arg Lys Arg Phe Leu
315 625                               630           635           640
318 Trp Gln His Gln Leu Leu Gly Leu Leu Ser Val Tyr Thr Arg Pro Ser
319                               645           650           655
322 Cys Gly Pro Glu Ala Leu Gly His Leu Leu Ser Arg Ala Arg Ser Pro
323                               660           665           670
326 Glu Glu Leu Ser Leu Ala Thr Gln Leu Tyr Ala Gly Leu Val Val Ser
327                               675           680           685
330 Leu Ser Gly Leu Leu Pro Leu Ala Phe Arg Ser Cys Leu Ala Arg Val
331                               690           695           700
334 His Ala Gly Thr Leu Gln Pro Pro Phe Thr Ala Arg Phe Leu Arg Asn
335 705                               710           715           720
338 Leu Ala Leu Leu Val Gly Trp Glu Gln Gln Gly Gly Glu Gly Pro Ala
339                               725           730           735
342 Ala Leu Gly Ala His Phe Gly Glu Ser Ala Ser Ala His Leu Ser Asp
343                               740           745           750
346 Leu Ala Pro Leu Leu Leu His Pro Glu Glu Glu Val Ala Glu Ala Ala
347                               755           760           765
350 Ala Ser Leu Leu Ala Ile Cys Pro Phe Pro Ser Glu Ala Leu Ser Pro
351                               770           775           780
354 Ser Gln Leu Leu Gly Leu Val Arg Ala Gly Val His Arg Phe Phe Ala
355 785                               790           795           800
358 Ser Leu Arg Leu His Gly Pro Pro Gly Val Ala Ser Ala Cys Gln Leu
359                               805           810           815
362 Leu Thr Arg Leu Ser Gln Thr Ser Pro Ala Gly Leu Lys Ala Val Leu
363                               820           825           830
366 Gln Leu Leu Val Glu Gly Ala Leu His Arg Gly Asn Thr Glu Leu Phe
367                               835           840           845
370 Gly Gly Gln Val Asp Gly Asp Asn Glu Thr Leu Ser Val Val Ser Ala

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371      850      855      860
374 Ser Leu Ala Ser Ala Ser Leu Leu Asp Thr Asn Arg Arg His Thr Ala
375 865      870      875      880
378 Ala Val Pro Gly Pro Gly Gly Ile Trp Ser Val Phe His Ala Gly Val
379      885      890      895
382 Ile Gly Arg Gly Leu Lys Pro Pro Lys Phe Val Gln Ser Arg Asn Gln
383      900      905      910
386 Gln Glu Val Ile Tyr Asn Thr Gln Ser Leu Leu Ser Leu Leu Val His
387      915      920      925
390 Cys Cys Ser Ala Pro Gly Gly Thr Glu Cys Gly Glu Cys Trp Gly Ala
391      930      935      940
394 Pro Ile Leu Ser Pro Glu Ala Ala Lys Ala Val Ala Val Thr Leu Val
395 945      950      955      960
398 Glu Ser Val Cys Pro Asp Ala Ala Gly Ala Glu Leu Ala Trp Pro Pro
399      965      970      975
402 Glu Glu His Ala Arg Ala Thr Val Glu Arg Asp Leu Arg Ile Gly Arg
403      980      985      990
406 Arg Phe Arg Glu Gln Pro Leu Leu Phe Glu Leu Leu Lys Leu Val Ala
407      995      1000      1005
410 Ala Ala Pro Pro Ala Leu Cys Tyr Cys Ser Val Leu Leu Arg Gly
411      1010      1015      1020
414 Leu Leu Ala Ala Leu Leu Gly His Trp Glu Ala Ser Arg His Pro
415      1025      1030      1035
418 Asp Thr Thr His Ser Pro Trp His Leu Glu Ala Ser Cys Thr Leu
419      1040      1045      1050
422 Val Ala Val Met Ala Glu Gly Ser Leu Leu Pro Pro Ala Leu Gly
423      1055      1060      1065
426 Asn Met His Glu Val Phe Ser Gln Leu Ala Pro Phe Glu Val Arg
427      1070      1075      1080
430 Leu Leu Leu Leu Ser Val Trp Gly Phe Leu Arg Glu His Gly Pro
431      1085      1090      1095
434 Leu Pro Gln Lys Phe Ile Phe Gln Ser Glu Arg Gly Arg Phe Ile
435      1100      1105      1110
438 Arg Asp Phe Ser Arg Glu Gly Gly Gly Glu Gly Gly Pro His Leu
439      1115      1120      1125
442 Ala Val Leu His Ser Val Leu His Arg Asn Ile Asp Arg Leu Gly
443      1130      1135      1140
446 Leu Phe Ser Gly Arg Phe Gln Ala Pro Ser Pro Ser Thr Leu Leu
447      1145      1150      1155
450 Arg Gln Gly Thr
451      1160
454 <210> SEQ ID NO: 3
455 <211> LENGTH: 1162
456 <212> TYPE: PRT
457 <213> ORGANISM: Artificial
459 <220> FEATURE:
460 <223> OTHER INFORMATION: A variant of the human BFLP1698 polypeptide
462 <400> SEQUENCE: 3
464 Met Ala Leu Val Pro Gly Arg Ser Lys Glu Asp Gly Leu Trp Thr Arg

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RAW SEQUENCE LISTING ERROR SUMMARY DATE: 09/07/2005
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Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete,
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:3,4,5,6,7,8,9,10,11,12,13,14

VERIFICATION SUMMARY

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